

295210.seq.list.substitute.txt
SEQUENCE LISTING

<110> KAO CORPORATION
Keiji Endo
Katsuya Ozaki

<120> Mutant Bacterium Belonging to the Genus Bacillus

<130> KS0816

<150> JP 2004-062852

<151> 2004-03-05

<160> 28

<170> PatentIn Ver. 3.1

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<213> Bacillus subtilis

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Met Asp Glu Tyr Tyr Glu Phe Leu Gly Glu Gln Gly Val Glu Leu Ile
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Ser Glu Asn Glu Glu Thr Glu Asp Pro Asn Ile Gln Gln Leu Ala Lys
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Ala Glu Glu Glu Phe Asp Leu Asn Asp Leu Ser Val Pro Pro Gly Val
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Trp Ile Arg Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr
 195 200 205

Ile Arg Ile Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg
 210 215 220

Val Gln Arg Gln Leu Leu Gln Asp Leu Gly Arg Glu Pro Thr Pro Glu
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Glu Ile Ala Glu Asp Met Asp Leu Thr Pro Glu Lys Val Arg Glu Ile
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Leu Lys Ile Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu
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Ser Pro Ser Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu
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295210.seq.list.substitute.txt

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Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
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 Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly
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 Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
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Page 7

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cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag	833
His Gly Glu Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln	45 50 55
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Trp Phe Pro Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn	60 65 70
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Asp Trp Asp Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn	75 80 85 90
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Gly Tyr Ala Thr Asn Pro Glu Leu Ile Lys Gln Arg Val Ile Asp Gly	95 100 105
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Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met 65 70 75 80			

295210.seq.list.substitute.txt

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
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Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
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Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
115 120 125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
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Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
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Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
165 170 175

Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
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Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
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Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
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Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
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Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
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Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
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Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
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Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
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Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
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Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp
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Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly
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Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
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Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile
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Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn
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Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met
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Gln Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val
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Glu Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu
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Thr Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His
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Ala Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu
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Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu
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Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro
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Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu
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Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn

580

585

590

Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn
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 660 665 670

Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val
 675 680 685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
 690 695 700

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Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
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Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
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cctgattttta ttttttttgaa ttttttttgag aactaaagat tgaaatagaa gtagaagaca    180
acggacataa gaaaattgta ttagtttttaa ttatagaaaa cgctttttcta taattatttta    240
tacctagaac gaaaatactg tttcgaaagc ggttttactat aaaaccttat attccggctc     300
ttttttttaa caggggggtga aaattcactc tagtatttcta atttcaacat gctataataa     360
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tatatgccga ttttaggaagg gggtagattg agtcaagtag tcataattta gataacttat     480
aagttgttga gaagcaggag agaatctggg ttactcacia gtttttttaa acattatcga     540
aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta     600
ggaggtaat atg atg tta aga aag aaa aca aag cag ttg att tct tcc att     651
      Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile
                    -25                    -20

ctt att tta gtt tta ctt cta tct tta ttt ccg aca gct ctt gca gca      699
Leu Ile Leu Val Leu Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala
-15                    -10                    -5                    -1 1

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aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc      795
Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val
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gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa tta      843
Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu
35                    40                    45

cgt gga atg agt aca cac gga tta caa tgg ttt cct gag atc ttg aat      891
Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn
50                    55                    60                    65

gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg att      939
Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile
70                    75                    80

cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca gag      987
Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu
85                    90                    95

tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa aat      1035

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Asp	Met	Tyr	Val	Ile	Val	Asp	Trp	His	Val	His	Ala	Pro	Gly	Asp	Pro		
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Arg	Asp	Pro	Val	Tyr	Ala	Gly	Ala	Glu	Asp	Phe	Phe	Arg	Asp	Ile	Ala		
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cca	agt	agt	aac	aat	aat	ggg	gga	gct	ggg	att	cca	aat	aat	gaa	gaa		1227
Pro	Ser	Ser	Asn	Asn	Asn	Gly	Gly	Ala	Gly	Ile	Pro	Asn	Asn	Glu	Glu		
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cgt	gat	agc	ggg	aac	gca	gat	gac	aat	att	atc	att	gtg	ggg	agt	cca		1323
Arg	Asp	Ser	Gly	Asn	Ala	Asp	Asp	Asn	Ile	Ile	Ile	Val	Gly	Ser	Pro		
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Asn	Trp	Ser	Gln	Arg	Pro	Asp	Leu	Ala	Ala	Asp	Asn	Pro	Ile	Asp	Asp		
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cac	cat	aca	atg	tat	act	gtt	cac	ttc	tac	act	ggg	tca	cat	gct	gct		1419
His	His	Thr	Met	Tyr	Thr	Val	His	Phe	Tyr	Thr	Gly	Ser	His	Ala	Ala		
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tca	act	gaa	agc	tat	ccg	cct	gaa	act	cct	aac	tct	gaa	aga	gga	aac		1467
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aca Thr 370	aaa Lys	tac Tyr	acg Thr	aaa Lys	gta Val 375	ctt Leu	tgg Trp	gac Asp	ttt Phe	aat Asn 380	gat Asp	gga Gly	acg Thr	aag Lys	caa Gln 385	1851
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gaa Glu	aat Asn 515	aac Asn	aac Asn	atc Ile	aac Asn	aac Asn 520	atc Ile	att Ile	ctt Leu	ttt Phe	gta Val 525	gga Gly	act Thr	gaa Glu	ggt Gly	2283
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ggt Gly	gtg Val	aaa Lys 580	aca Thr	gct Ala	tta Leu	aca Thr	att Ile 585	gaa Glu	gaa Glu	gca Ala	aac Asn	ggt Gly 590	tct Ser	aac Asn	gcg Ala	2475
tta Leu	tca Ser 595	tgg Trp	gaa Glu	ttt Phe	gga Gly	tac Tyr 600	cca Pro	gaa Glu	gta Val	aaa Lys	cct Pro 605	agt Ser	gat Asp	aac Asn	tgg Trp	2523

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aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg 710 715 720	2859
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 <220>
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 <210> 17
 <211> 42
 <212> DNA
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 <220>
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 and 5'-portion from sigA in Bacillus subtilis; the sequence containing a
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Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu Ser Asp	20 25 30
gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt aat agt	424
Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser	35 40 45 50
cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag	472
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	55 60 65
ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag gca cag	520
Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln	70 75 80
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gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg gag gca	616
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tac Tyr 195	ctg Leu	tta Leu	gga Gly	tcg Ser	aat Asn 200	atc Ile	gac Asp	ttt Phe	agt Ser	cat His 205	cca Pro	gaa Glu	gta Val	caa Gln	gat Asp 210	904
gag Glu	ttg Leu	aag Lys	gat Asp	tgg Trp 215	ggg Gly	agc Ser	tgg Trp	ttt Phe	acc Thr 220	gat Asp	gag Glu	tta Leu	gat Asp	ttg Leu 225	gat Asp	952
ggg Gly	tat Tyr	cgt Arg	tta Leu 230	gat Asp	gct Ala	att Ile	aaa Lys	cat His 235	att Ile	cca Pro	ttc Phe	tgg Trp	tat Tyr 240	aca Thr	tct Ser	1000
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gta Val	ggg Gly 260	gaa Glu	tat Tyr	tgg Trp	aag Lys	gat Asp 265	gac Asp	gta Val	ggg Gly	gct Ala	ctc Leu 270	gaa Glu	ttt Phe	tat Tyr	tta Leu	1096
gat Asp 275	gaa Glu	atg Met	aat Asn	tgg Trp	gag Glu 280	atg Met	tct Ser	cta Leu	ttc Phe	gat Asp 285	ggt Val	cca Pro	ctt Leu	aat Asn	tat Tyr 290	1144
aat Asn	ttt Phe	tac Tyr	cgg Arg	gct Ala 295	tca Ser	caa Gln	caa Gln	ggg Gly	gga Gly 300	agc Ser	tat Tyr	gat Asp	atg Met	cgt Arg 305	aat Asn	1192
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ttt Phe	ggt Val	gat Asp 325	aat Asn	cat His	gat Asp	act Thr	cag Gln 330	cca Pro	ggg Gly	gag Glu	tca Ser	tta Leu 335	gag Glu	tca Ser	tgg Trp	1288
ggt Val	gct Ala 340	gat Asp	tgg Trp	ttt Phe	aag Lys	cca Pro 345	ctt Leu	gct Ala	tat Tyr	gcg Ala 350	aca Thr	att Ile	ttg Leu	acg Thr	cgt Arg	1336
gaa Glu	ggg Gly	ggg Gly	tat Tyr	cca Pro	aat Asn	gta Val	ttt Phe	tac Tyr	ggg Gly	gat Asp	tac Tyr	tat Tyr	ggg Gly	att Ile	cct Pro	1384

355	360	365	370	
aac gat aac att tca gct aaa aaa gat atg att gat gag ctg ctt gat	Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu Leu Asp			1432
	375	380	385	
gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt gat cat	Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His			1480
	390	395	400	
tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga cct aat	Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg Pro Asn			1528
	405	410	415	
tca ggc ctt gcg act att atg tgc aat gga cct ggt ggt tcc aag tgg	Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp			1576
	420	425	430	
atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat tta act	Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr			1624
	435	440	445	450
ggt aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa	Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu			1672
	455	460	465	
ttc ttt acg aat gga gga tct gta tcc gtg tac gtg aac caa taacaaaaa	Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln			1723
	470	475	480	
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tctacgactt tg				1795

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Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
Page 23

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
 100 105 110
 Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
 115 120 125
 Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
 130 135 140
 Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
 145 150 155 160
 Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
 165 170 175
 Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
 195 200 205
 Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
 210 215 220
 Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
 225 230 235 240
 Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
 245 250 255
 Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
 260 265 270
 Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
 275 280 285
 Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
 290 295 300
 Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
 325 330 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
340 345 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
355 360 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385 390 395 400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
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Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
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taccagcttg gacgagttgg gataaaagtg aggaggggaac cga atg aag aaa ccg 175
Met Lys Lys Pro
1

ttg ggg aaa att gtc gca agc acc gca cta ctc att tct gtt gct ttt 223
Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile Ser Val Ala Phe
5 10 15 20

agt tca tcg atc gca tcg gct gct gag gaa gca aaa gaa aaa tat tta 271
Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys Glu Lys Tyr Leu
25 30 35

att ggc ttt aat gag cag gaa gca gtt agt gag ttt gta gag caa ata 319
Page 25

Ile	Gly	Phe	Asn	Glu	Gln	Glu	Ala	Val	Ser	Glu	Phe	Val	Glu	Gln	Ile		
			40					45					50				
gag	gca	aat	gac	gat	gtc	gcg	att	ctc	tct	gag	gaa	gag	gaa	gtc	gaa	367	
Glu	Ala	Asn	Asp	Asp	Val	Ala	Ile	Leu	Ser	Glu	Glu	Glu	Glu	Val	Glu		
		55					60					65					
att	gaa	ttg	ctt	cat	gag	ttt	gaa	acg	att	cct	gtt	tta	tct	gtt	gag	415	
Ile	Glu	Leu	Leu	His	Glu	Phe	Glu	Thr	Ile	Pro	Val	Leu	Ser	Val	Glu		
	70					75					80						
tta	agt	cca	gaa	gat	gtg	gac	gcg	ctt	gag	ctc	gat	cca	acg	att	tcg	463	
Leu	Ser	Pro	Glu	Asp	Val	Asp	Ala	Leu	Glu	Leu	Asp	Pro	Thr	Ile	Ser		
85					90					95					100		
tat	att	gaa	gag	gat	gca	gaa	gta	acg	aca	atg	gcg	caa	tca	gtg	cca	511	
Tyr	Ile	Glu	Glu	Asp	Ala	Glu	Val	Thr	Thr	Met	Ala	Gln	Ser	Val	Pro		
				105					110					115			
tgg	gga	att	agc	cgt	gta	caa	gcc	cca	gct	gcc	cat	aac	cgt	gga	ttg	559	
Trp	Gly	Ile	Ser	Arg	Val	Gln	Ala	Pro	Ala	Ala	His	Asn	Arg	Gly	Leu		
			120					125					130				
aca	ggt	tct	ggt	gta	aaa	gtt	gct	gtc	ctc	gat	acg	ggt	att	tcc	acc	607	
Thr	Gly	Ser	Gly	Val	Lys	Val	Ala	Val	Leu	Asp	Thr	Gly	Ile	Ser	Thr		
		135					140					145					
cat	cca	gac	tta	aat	att	cgc	ggt	ggt	gct	agc	ttt	gtg	cca	gga	gaa	655	
His	Pro	Asp	Leu	Asn	Ile	Arg	Gly	Gly	Ala	Ser	Phe	Val	Pro	Gly	Glu		
	150					155					160						
cca	tcc	act	caa	gat	gga	aat	gga	cat	ggc	acg	cat	gtg	gca	ggg	acg	703	
Pro	Ser	Thr	Gln	Asp	Gly	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Thr		
165					170					175					180		
att	gct	gct	tta	aac	aat	tcg	att	ggc	gtt	ctg	ggc	gta	gca	ccg	agc	751	
Ile	Ala	Ala	Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	Ser		
				185					190					195			
gcg	gaa	cta	tac	gct	gta	aaa	gta	tta	ggc	gcg	agc	ggt	tca	ggt	tcg	799	
Ala	Glu	Leu	Tyr	Ala	Val	Lys	Val	Leu	Gly	Ala	Ser	Gly	Ser	Gly	Ser		
			200					205					210				
gtc	agc	tcg	att	gcc	caa	gga	ttg	gaa	tgg	gca	ggg	aac	aat	ggc	atg	847	
Val	Ser	Ser	Ile	Ala	Gln	Gly	Leu	Glu	Trp	Ala	Gly	Asn	Asn	Gly	Met		
		215					220					225					
cac	gtt	gcg	aat	ttg	agt	tta	gga	agc	ccg	tcg	ccg	agt	gca	aca	ctt	895	
His	Val	Ala	Asn	Leu	Ser	Leu	Gly	Ser	Pro	Ser	Pro	Ser	Ala	Thr	Leu		
	230					235					240						
gag	caa	gct	gtt	aat	agc	gct	act	tct	aga	ggc	gtt	ctt	gtc	gta	gca	943	
Glu	Gln	Ala	Val	Asn	Ser	Ala	Thr	Ser	Arg	Gly	Val	Leu	Val	Val	Ala		
245					250					255					260		
gca	tct	ggt	aat	tca	ggt	gca	ggc	tca	atc	agc	tat	ccg	gcc	cgt	tat	991	
Ala	Ser	Gly	Asn	Ser	Gly	Ala	Gly	Ser	Ile	Ser	Tyr	Pro	Ala	Arg	Tyr		
				265					270					275			
gcg	aac	gca	atg	gca	gtc	gga	gcg	act	gac	caa	aac	aac	aac	cgc	gct	1039	
Ala	Asn	Ala	Met	Ala	Val	Gly	Ala	Thr	Asp	Gln	Asn	Asn	Asn	Arg	Ala		
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 Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val Ala Pro Gly Val
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 Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala Ser Leu Asn Gly
 310 315 320

aca tcg atg gct act cct cat gtt gca ggt gta gca gcc ctt gtt aaa 1183
 Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala Ala Leu Val Lys
 325 330 335 340

caa aag aat cca tct tgg tcc aat gta caa atc cgc aat cat cta aag 1231
 Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg Asn His Leu Lys
 345 350 355

aat acg gca acg ggt tta gga aac acg aac ttg tat gga agc ggg ctt 1279
 Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr Gly Ser Gly Leu
 360 365 370

gtc aat gca gaa gcg gca aca cgc taatcaataa taataacgct gtgtgcttta 1333
 Val Asn Ala Glu Ala Ala Thr Arg
 375 380

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aaagcgagcg taaagggcta ttgaagctct ttacgcttgc aggatttg 1441

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 <213> Bacillus clausii KSM-K16

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 20 25 30

Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe
 35 40 45

Val Glu Gln Ile Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu
 50 55 60

Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val
 65 70 75 80

Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp
 85 90 95

Pro Thr Ile Ser Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala
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295210.seq.list.substitute.txt

Gln Ser Val₁₁₅ Pro Trp Gly Ile Ser₁₂₀ Arg Val Gln Ala Pro₁₂₅ Ala Ala His

Asn Arg₁₃₀ Gly Leu Thr Gly Ser₁₃₅ Gly Val Lys Val Ala₁₄₀ Val Leu Asp Thr

Gly₁₄₅ Ile Ser Thr His Pro₁₅₀ Asp Leu Asn Ile Arg₁₅₅ Gly Gly Ala Ser Phe₁₆₀

Val Pro Gly Glu Pro₁₆₅ Ser Thr Gln Asp Gly₁₇₀ Asn Gly His Gly Thr His₁₇₅

Val Ala Gly Thr₁₈₀ Ile Ala Ala Leu Asn₁₈₅ Asn Ser Ile Gly Val₁₉₀ Leu Gly

Val Ala Pro₁₉₅ Ser Ala Glu Leu Tyr₂₀₀ Ala Val Lys Val Leu₂₀₅ Gly Ala Ser

Gly Ser₂₁₀ Gly Ser Val Ser Ser₂₁₅ Ile Ala Gln Gly Leu₂₂₀ Glu Trp Ala Gly

Asn Asn Gly Met His Val₂₃₀ Ala Asn Leu Ser Leu₂₃₅ Gly Ser Pro Ser Pro₂₄₀

Ser Ala Thr Leu Glu₂₄₅ Gln Ala Val Asn Ser₂₅₀ Ala Thr Ser Arg Gly₂₅₅ Val

Leu Val Val Ala₂₆₀ Ala Ser Gly Asn Ser₂₆₅ Gly Ala Gly Ser Ile₂₇₀ Ser Tyr

Pro Ala Arg₂₇₅ Tyr Ala Asn Ala Met₂₈₀ Ala Val Gly Ala Thr₂₈₅ Asp Gln Asn

Asn Asn Arg Ala Ser Phe Ser₂₉₅ Gln Tyr Gly Ala Gly₃₀₀ Leu Asp Ile Val

Ala Pro Gly Val Asn Val₃₁₀ Gln Ser Thr Tyr Pro₃₁₅ Gly Ser Thr Tyr Ala₃₂₀

Ser Leu Asn Gly Thr₃₂₅ Ser Met Ala Thr Pro₃₃₀ His Val Ala Gly Val₃₃₅ Ala

Ala Leu Val Lys₃₄₀ Gln Lys Asn Pro Ser₃₄₅ Trp Ser Asn Val Gln₃₅₀ Ile Arg

Asn His Leu₃₅₅ Lys Asn Thr Ala Thr₃₆₀ Gly Leu Gly Asn Thr₃₆₅ Asn Leu Tyr

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 upstream region of alkaline cellulase gene in *Bacillus* sp. KSM-S237

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<210> 23
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer designed from the downstream region of the
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 BglII restriction site at the 5'-end

<400> 23
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<210> 24
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer designed from the upstream region of the
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 BamHI restriction site at the 5'-end

<400> 24
 cccggatcca acaggcttat attta 25

<210> 25
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 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer; 3'-portion from the upstream region of the
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 from the alkaline protease gene in *Bacillus clausii* KSM-K16

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<210> 26
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer; 3'-portion from nucleotide
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 38; 5'-portion from the alkaline cellulase gene in Bacillus sp. KSM-S237

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<210> 27
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 <223> Oligonucleotide as PCR primer designed from the downstream region of the
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 xbaI restriction site at the 5'-end

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<210> 28
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer; its 3'-portion designed from the alkaline
 cellulase gene in Bacillus sp. KSM-S237 and its 5'-portion designed from the
 alkaline amylase gene in Bacillus sp. KSM-K38

<400> 28
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